

1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808

Wood, William I.

<151> February 9, 1999

[illegible]

<150> 60/119,965

<150> 60/162,506

<150> 60/170,262

<150> 60/187,202

<150> PCT/US99/12252

<150> PCT/US99/28634

<150> PCT/US99/28551

<150> PCT/US00/03565

<150> PCT/US00/04414

<150> PCT/US00/05841

<150> PCT/US00/08439

<150> PCT/US00/14941

<150> PCT/US00/15264

<150> PCT/US00/32678

<160> 38

<210> 1

<211> 1283

<212> DNA

<213> Homo sapiens

<400> 1

cggacgcgtg ggaccatac ttgctgtct gatccatgca caaggcgggg 50
ctgctaggcc tctgtgcccg ggcttgaat tcggtgcgga tggccagctc 100
cgggatgacc cgccgggacc cgctcgaaa taaggtggcc ctgtaacgg 150
cctccaccga cgggatcggc ttcgcatcg cccggcgttt ggcccaggac 200
ggggcccatg tggtcgtcag cagccggaag cagcagaatg tggaccaggc 250
ggtggccacg ctgcaggggg aggggctgag cgtgacgggc accgtgtgcc 300
atgtggggaa ggcggaggac cgggagcggc tggtgccac ggctgtgaag 350
cttcattgag gtatcgatat cctagtctcc aatgctgctg tcaacccttt 400
ctttggaagc ataatggatg tcaactagga ggtgtgggac aagactctgg 450
acattaatgt gaaggcccca gccctgatga caaaggcagt ggtgccagaa 500
atggagaaac gaggaggcgg ctcaagtgtg atcgtgtctt ccatagcagc 550
cttcagtcca tctcctggct tcagtcctta caatgtcagt aaaacagcct 600
tgctgggcct gaccaagacc ctggccatag agctggcccc aaggaacatt 650
agggtgaact gcctagcacc tggacttatc aagactagct tcagcaggat 700
gctctggatg gacaaggaaa aagaggaaag catgaaagaa accctgcgga 750
taagaagggt aggcgagcca gaggattgtg ctggcatcgt gtctttctg 800
tgctctgaag atgccagcta catcactggg gaaacagtgg tggtggtgg 850
aggaaccccg tcccgcctct gaggaccggg agacagccca caggccagag 900
ttgggtcta gctcctggtg ctgttctgc attcaccac tggcctttcc 950

cacctctgct caccttactg ttcacctcat caaatcagtt ctgccctgtg 1000
aaaagatcca gccttcctg ccgtcaaggt ggcgctttac tcgggattcc 1050
tgctgttgtt gtggccttgg gtaaaggcct cccctgagaa cacaggacag 1100
gcctgtgac aaggctgagt ctaccttggc aaagaccaag atatttttc 1150
ctgggccact ggtgaatctg aggggtgatg ggagagaagg aacctggagt 1200
ggaaggagca gagttgcaaa ttaacagctt gcaaagagg tgcaaataaa 1250
atgcagatga ttgcgcggct ttgaaaaaaa aaa 1283

<210> 2

<211> 278

<212> PRT

<213> Homo sapiens

<400> 2

Met	His	Lys	Ala	Gly	Leu	Leu	Gly	Leu	Cys	Ala	Arg	Ala	Trp	Asn
1		5		10				15						
Ser	Val	Arg	Met	Ala	Ser	Ser	Gly	Met	Thr	Arg	Arg	Asp	Pro	Leu
		20			25			30						
Ala	Asn	Lys	Val	Ala	Leu	Val	Thr	Ala	Ser	Thr	Asp	Gly	Ile	Gly
		35			40			45						
Phe	Ala	Ile	Ala	Arg	Arg	Leu	Ala	Gln	Asp	Gly	Ala	His	Val	Val
		50			55			60						
Val	Ser	Ser	Arg	Lys	Gln	Gln	Asn	Val	Asp	Gln	Ala	Val	Ala	Thr
		65			70			75						
Leu	Gln	Gly	Glu	Gly	Leu	Ser	Val	Thr	Gly	Thr	Val	Cys	His	Val
		80			85			90						
Gly	Lys	Ala	Glu	Asp	Arg	Glu	Arg	Leu	Val	Ala	Thr	Ala	Val	Lys
		95			100			105						
Leu	His	Gly	Gly	Ile	Asp	Ile	Leu	Val	Ser	Asn	Ala	Ala	Val	Asn
		110			115			120						
Pro	Phe	Phe	Gly	Ser	Ile	Met	Asp	Val	Thr	Glu	Glu	Val	Trp	Asp

125 130 135

Lys Thr Leu Asp Ile Asn Val Lys Ala Pro Ala Leu Met Thr Lys
140 145 150

Ala Val Val Pro Glu Met Glu Lys Arg Gly Gly Gly Ser Val Val
155 160 165

Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser Pro Gly Phe Ser
170 175 180

Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu Thr Lys Thr
185 190 195

Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn Cys Leu
200 205 210

Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp Met
215 220 225

Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
230 235 240

Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu
245 250 255

Cys Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val
260 265 270

Gly Gly Gly Thr Pro Ser Arg Leu
275

<210> 3

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic Oligonucleotide Probe

<400> 3

gcataatgga tgcactgag g 21

<210> 4
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic Oligonucleotide Probe

<400> 4
agaacaatcc tgctgaaagc tag 23

<210> 5
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic Oligonucleotide Probe

<400> 5
gaaacgagga ggcggctcag tggatgatcgt gtcttcata gcagcc 46

<210> 6
<211> 3121
<212> DNA
<213> Homo sapiens

<400> 6
gcgcctgag ctccgctcc gggcccgata gcggcatcga gagegcctcc 50

gtcgaggacc aggcggcgca gggggccggc gggcgaaagg aggatgaggg 100

ggcgcagcag ctgctgacct tgcagaacca ggtggcgcggt ctggaggagg 150

agaaccgaga cttctggct gcgctggagg acgcatgga gcagtacaaa 200

ctgcagagcg accggctgctg tgagcagcag gaggagatgg tggactgctg 250

gctgcgggta gagctggctg ggccaggctg ggggggcctg cggctcctga 300

atggcctgcc tcccgggtcc ttgtgcctc gacctatac agccccctg 350

gggggtgcc acgcccattg gctgggcatg gtccgcctg cctgcctccc 400
 tggagatgaa gttggctctg agcagagggg agagcaggtg acaaatggca 450
 gggaggctgg agctgagttg ctgactgagg tgaacaggct gggaagtggc 500
 tcttcagctg cttcagagga ggaagaggag gaggaggagc cgcccaggcg 550
 gaccttacac ctgcgcagaa ataggatcag caactgcagt cagagggcgg 600
 gggcacgccc agggagtctg ccagagagga agggcccaga gctttgcctt 650
 gaggagtgg atgcagccat tccagggtcc agagcagttg gtgggagcaa 700
 ggcccagatt caggcccgc aggtccccc tgccacagcc tcagagtggc 750
 ggctggccca ggcccagcag aagatccggg agctggctat caacatccgc 800
 atgaaggagg agcttattgg cgagctggc cgcacaggaa aggcagctca 850
 ggccctgaac cgccagcaca gccagcgtat ccgggagctg gacagaggag 900
 cagagcaggt gcgggcccag ctgagtgaag gccagaggca gctgcgggag 950
 ctcgagggca aggagctcca ggatgctggc gagcggctc ggctccagga 1000
 gttccgagg agggctgctg cgcccagag ccaggtgcag gtgctgaagg 1050
 agaagaagca ggctacggag cggtgtgtgt cactgtcggc ccagagttag 1100
 aagcgactgc aggagctcga gcggaactg cagctcatgc ggcagcagca 1150
 gggacagctg cagaggcggc ttgcgagga gacggagcag aagcggcgcc 1200
 tggaggcaga aatgagcaag cggcagcacc gcgtcaagga gctggagctg 1250
 aagcatgagc aacagcagaa gatcctgaag attaagacgg aagagatcgc 1300
 ggccttccag aggaagaggc gcagtggcag caacggctct gtggtcagcc 1350
 tggaacagca gcagaagatt gaggagcaga agaagtggct ggaccaggag 1400
 atggagaagg tgctacagca gcggcgggcg ctggaggagc tgggggagga 1450
 getccacaag cgggaggcca tcttgccaa gaaggaggcc ctgatgcagg 1500

agaagacggg gctggagagc aagcgccctga gatccagcca ggccctcaac 1550
gaggacatcg tgcgagtgtc cagccggctg gagcacctgg agaaggagct 1600
gtccgagaag agcggggcagc tgcggcaggg cagcgcccag agccagcagc 1650
agatccgcgg ggagatcgac agcctgcgcc aggagaagga ctgctgctc 1700
aagcagcgcc tggagatcga cggcaagctg aggcagggga gtctgctgtc 1750
ccccaggag gagcggacgc tgtccagtt ggatgaggcc atcagggcc 1800
tgatgctgc cattgagtat aagaatgagg ccatcacatg ccgccagcgg 1850
gtgttcggg cctcagctc gttgctgtcc cagtgcgaga tgaacctcat 1900
ggccaagctc agctacctt catctcaga gaccagagcc ctctctgca 1950
agtatttga caaggtggtg acgtccgag aggagcagca ccagcagcag 2000
attgccttct cggaactgga gatgcagctg gaggagcagc agaggctggt 2050
gtactggctg gaggtggccc tggagcggca ggcctggag atggaccgcc 2100
agtgaccct gcagcagaag gagcacgagc agaacatgca gctgctcctg 2150
cagcagagtc gagaccact cgggaaggg ttagcagaca gcaggaggca 2200
gtatgaggcc cggattcaag ctctggagaa ggaactgggc cgttacatgt 2250
ggataaacca ggaactgaaa cagaagctcg gcggtgtgaa cgctgtaggc 2300
cacagcaggg gtggggagaa gaggagcctg tgctcggagg gcagacaggc 2350
tcctggaaat gaagatgagc tccacctggc acccgagctt ctctggctgt 2400
ccccctcac tgagggggcc ccccgaccc gggaggagac gcgggacttg 2450
gtccacgtc cgttacctt gacctggaaa cgctcgagcc tgtgtggtga 2500
ggagcagggg tccccgagg aactgaggca gcgggaggcg gctgagcccc 2550
tggtggggcg ggtgcttct gtgggtgagg caggcctgcc ctggaacttt 2600
gggcctttgt ccaagccccg gcgggaactg cgacagacca gcccggggat 2650

gattgatgtc cggaaaaacc ccctgtaagc cctcggggca gaccctgcct 2700

tggagggaga ctccgagcct gctgaaaggg gcagctgcct gttttgcttc 2750

tgtgaagggc agtccttacc gcacacccta aatccaggcc ctcatctgta 2800

ccctcactgg gatcaacaaa ttggggccat ggcccaaaag aactggaccc 2850

tcatttaaca aaataatatg caaatccca ccacttactt ccatgaagct 2900

gtgttaccca attgccgcct tgtgtcttgc tcgaatctca ggacaattct 2950

ggtttcaggc gtaaatggat gtgctttag ttcaggggtt tggccaagaa 3000

tcatcacgaa agggtcgggtg gcaaccaggt tgtggtttaa atggtcttat 3050

gtatataggg gaaactggga gacttagga tcttaaaaaa ccatttaata 3100

aaaaaaaaatc ttgaaggga c 3121

<210> 7

<211> 830

<212> PRT

<213> Homo sapiens

<400> 7

Met Glu Gln Tyr Lys Leu Gln Ser Asp Arg Leu Arg Glu Gln Gln

1 5 10 15

Glu Glu Met Val Glu Leu Arg Leu Arg Leu Glu Leu Val Arg Pro

20 25 30

Gly Trp Gly Gly Leu Arg Leu Leu Asn Gly Leu Pro Pro Gly Ser

35 40 45

Phe Val Pro Arg Pro His Thr Ala Pro Leu Gly Gly Ala His Ala

50 55 60

His Val Leu Gly Met Val Pro Pro Ala Cys Leu Pro Gly Asp Glu

65 70 75

Val Gly Ser Glu Gln Arg Gly Glu Gln Val Thr Asn Gly Arg Glu

80 85 90

Ala Gly Ala Glu Leu Leu Thr Glu Val Asn Arg Leu Gly Ser Gly

95	100	105
Ser Ser Ala Ala Ser Glu Glu Glu Glu Glu Glu Glu Glu Pro Pro		
110	115	120
Arg Arg Thr Leu His Leu Arg Arg Asn Arg Ile Ser Asn Cys Ser		
125	130	135
Gln Arg Ala Gly Ala Arg Pro Gly Ser Leu Pro Glu Arg Lys Gly		
140	145	150
Pro Glu Leu Cys Leu Glu Glu Leu Asp Ala Ala Ile Pro Gly Ser		
155	160	165
Arg Ala Val Gly Gly Ser Lys Ala Arg Val Gln Ala Arg Gln Val		
170	175	180
Pro Pro Ala Thr Ala Ser Glu Trp Arg Leu Ala Gln Ala Gln Gln		
185	190	195
Lys Ile Arg Glu Leu Ala Ile Asn Ile Arg Met Lys Glu Glu Leu		
200	205	210
Ile Gly Glu Leu Val Arg Thr Gly Lys Ala Ala Gln Ala Leu Asn		
215	220	225
Arg Gln His Ser Gln Arg Ile Arg Glu Leu Glu Gln Glu Ala Glu		
230	235	240
Gln Val Arg Ala Glu Leu Ser Glu Gly Gln Arg Gln Leu Arg Glu		
245	250	255
Leu Glu Gly Lys Glu Leu Gln Asp Ala Gly Glu Arg Ser Arg Leu		
260	265	270
Gln Glu Phe Arg Arg Arg Val Ala Ala Ala Gln Ser Gln Val Gln		
275	280	285
Val Leu Lys Glu Lys Lys Gln Ala Thr Glu Arg Leu Val Ser Leu		
290	295	300
Ser Ala Gln Ser Glu Lys Arg Leu Gln Glu Leu Glu Arg Asn Val		
305	310	315
Gln Leu Met Arg Gln Gln Gln Gly Gln Leu Gln Arg Arg Leu Arg		

320 325 330

Glu Glu Thr Glu Gln Lys Arg Arg Leu Glu Ala Glu Met Ser Lys
335 340 345

Arg Gln His Arg Val Lys Glu Leu Glu Leu Lys His Glu Gln Gln
350 355 360

Gln Lys Ile Leu Lys Ile Lys Thr Glu Glu Ile Ala Ala Phe Gln
365 370 375

Arg Lys Arg Arg Ser Gly Ser Asn Gly Ser Val Val Ser Leu Glu
380 385 390

Gln Gln Gln Lys Ile Glu Glu Gln Lys Lys Trp Leu Asp Gln Glu
395 400 405

Met Glu Lys Val Leu Gln Gln Arg Arg Ala Leu Glu Glu Leu Gly
410 415 420

Glu Glu Leu His Lys Arg Glu Ala Ile Leu Ala Lys Lys Glu Ala
425 430 435

Leu Met Gln Glu Lys Thr Gly Leu Glu Ser Lys Arg Leu Arg Ser
440 445 450

Ser Gln Ala Leu Asn Glu Asp Ile Val Arg Val Ser Ser Arg Leu
455 460 465

Glu His Leu Glu Lys Glu Leu Ser Glu Lys Ser Gly Gln Leu Arg
470 475 480

Gln Gly Ser Ala Gln Ser Gln Gln Gln Ile Arg Gly Glu Ile Asp
485 490 495

Ser Leu Arg Gln Glu Lys Asp Ser Leu Leu Lys Gln Arg Leu Glu
500 505 510

Ile Asp Gly Lys Leu Arg Gln Gly Ser Leu Leu Ser Pro Glu Glu
515 520 525

Glu Arg Thr Leu Phe Gln Leu Asp Glu Ala Ile Glu Ala Leu Asp
530 535 540

Ala Ala Ile Glu Tyr Lys Asn Glu Ala Ile Thr Cys Arg Gln Arg

545 550 555

Val Leu Arg Ala Ser Ala Ser Leu Leu Ser Gln Cys Glu Met Asn
560 565 570

Leu Met Ala Lys Leu Ser Tyr Leu Ser Ser Ser Glu Thr Arg Ala
575 580 585

Leu Leu Cys Lys Tyr Phe Asp Lys Val Val Thr Leu Arg Glu Glu
590 595 600

Gln His Gln Gln Gln Ile Ala Phe Ser Glu Leu Glu Met Gln Leu
605 610 615

Glu Glu Gln Gln Arg Leu Val Tyr Trp Leu Glu Val Ala Leu Glu
620 625 630

Arg Gln Arg Leu Glu Met Asp Arg Gln Leu Thr Leu Gln Gln Lys
635 640 645

Glu His Glu Gln Asn Met Gln Leu Leu Leu Gln Gln Ser Arg Asp
650 655 660

His Leu Gly Glu Gly Leu Ala Asp Ser Arg Arg Gln Tyr Glu Ala
665 670 675

Arg Ile Gln Ala Leu Glu Lys Glu Leu Gly Arg Tyr Met Trp Ile
680 685 690

Asn Gln Glu Leu Lys Gln Lys Leu Gly Gly Val Asn Ala Val Gly
695 700 705

His Ser Arg Gly Gly Glu Lys Arg Ser Leu Cys Ser Glu Gly Arg
710 715 720

Gln Ala Pro Gly Asn Glu Asp Glu Leu His Leu Ala Pro Glu Leu
725 730 735

Leu Trp Leu Ser Pro Leu Thr Glu Gly Ala Pro Arg Thr Arg Glu
740 745 750

Glu Thr Arg Asp Leu Val His Ala Pro Leu Pro Leu Thr Trp Lys
755 760 765

Arg Ser Ser Leu Cys Gly Glu Glu Gln Gly Ser Pro Glu Glu Leu

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

cagctcccct tcccgetgag agccactttc atcggcaata aaatccccca 650

catttaccat ct 662

<210> 9
<211> 125
<212> PRT
<213> Homo sapiens

<400> 9
Met Arg Pro Arg Cys Cys Ile Leu Ala Leu Val Cys Trp Ile Thr
1 5 10 15

Val Phe Leu Leu Gln Cys Ser Lys Gly Thr Thr Asp Ala Pro Val
20 25 30

Gly Ser Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn
35 40 45

Lys Ile Tyr Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile
50 55 60

Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe
65 70 75

Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln
80 85 90

Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln
95 100 105

Cys His Leu Ser Pro Ile Ser Arg Ser Cys Thr Arg Asn Arg Arg
110 115 120

His Val Leu Tyr Pro
125

<210> 10
<211> 1942
<212> DNA
<213> Homo sapiens

<400> 10
ccccacgcgc cgcccacgcg tccgggtgcc actcgcgcgc cggccgcgct 50

ccgggttct ctttccctc cgacgcgcca cggtgccca gacattccgg 100

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

ctgccgggtc tggagagctc cccgaacccc tccgcggaga ggagcgaggc 150
ggcgccaggg tggccccgg ggcgcgttg gtctcggaga agcggggacg 200
aggccggagg atgagcgact gagggcgacg cgggcactga cgcgagtgg 250
ggccgcgact accggcagct gacagcgca tgagcgactc cccagagacg 300
ccctagcccc gtgtgcgcgc caggcggagc gcgcaggtgg ggctgggctg 350
ttagtggtcc gcccacgcg ggtcgccggc cggcccagga tggcgctgg 400
caaccgggc ccgcgccgc cgctgctacc cctgcgccg ctgcgagccc 450
ggcgtccggc ccgcgccctg cgctcatgga cggcggtcc cggctggcgg 500
cggcgcccc ccgggctgtg aatgcgactc gccctcggc cgcgtcccc 550
gcccgccgc ccgccgggac gtggtagggg atgccagct cactgcat 600
ggcagttggc gcgcttcca gtccctct ggtcacctgc tgcctgatgg 650
tggctctgt cagtccgagc atcccgtgg agaagctggc ccaggcacca 700
gagcagccgg gccaggagaa gcgtgagcac gccactcggg acggcccggg 750
gcgggtgaac gagctcgggc gcccggcgag ggacgagggc ggacgcggcc 800
gggactggaa gagcaagagc ggccgtgggc tcgccggccg tgagccgtgg 850
agcaagetga agcaggcctg ggtctccag ggcgggggcg ccaaggccgg 900
ggatctgcag gtccggcccc gcggggacac cccgcaggcg gaagccctgg 950
ccgcagccgc ccaggacgcg attggcccgg aactcgcgc cagcccag 1000
ccaccgagg agtacgtgta cccggactac cgtggcaagg gctgcgtgga 1050
cgagagcggc ttcgtgtacg cgatcgggga gaagttcgcg cggggccct 1100
cggcctgccc gtgcctgtgc accgaggagg ggccgctgt cgcgcagccc 1150
gagtgccega ggctgcaccc gcgtgcac cagtcgaca cgagccagt 1200
ctccccgag tgcaaggaga ggaagaacta ctgcgagttc cggggcaaga 1250

cctatcagac ttggaggag ttcgtggtgt ctccatgcga gaggtgtcgc 1300
 tgtgaagcca acggtgaggt gctatgcaca gtgtcagcgt gtccccagac 1350
 ggagtgtgtg gacctgtgt acgagcctga tcagtgtgt cccatctgca 1400
 aaaatggtcc aaactgcttt gcagaaaccg cggatgccc tgctggcaga 1450
 gaagtgaaga ctgacgagtg caccatatgc cactgtactt atgaggaagg 1500
 cacatggaga atcgagcggc aggccatgtg cacgagacat gaatgcaggc 1550
 aaatgtagac gcttcccaga acacaaactc tgacttttc tagaacattt 1600
 tactgatgtg aacattctag atgactctgg gaactatcag tcaaagaaga 1650
 cttttgatga ggaataatgg aaaattgttg gtactttcc tttcttgat 1700
 aacagtact acaacagaag gaaatggata tatttcaaaa catcaacaag 1750
 aactttgggc ataaaatcct tctctaaata aatgtgctat ttccacagta 1800
 agtacacaaa agtacactat tatatatcaa atgtattct ataatccctc 1850
 cattagagag cttatataag tgttttctat agatgcagat taaaaatgct 1900
 gtgtgtcaa ccgtcaaaaa aaaaaaaaaa aaaaaaaaaa aa 1942

<210> 11
 <211> 325
 <212> PRT
 <213> Homo sapiens

<400> 11
 Met Pro Ser Ser Thr Ala Met Ala Val Gly Ala Leu Ser Ser Ser
 1 5 10 15
 Leu Leu Val Thr Cys Cys Leu Met Val Ala Leu Cys Ser Pro Ser
 20 25 30
 Ile Pro Leu Glu Lys Leu Ala Gln Ala Pro Glu Gln Pro Gly Gln
 35 40 45
 Glu Lys Arg Glu His Ala Thr Arg Asp Gly Pro Gly Arg Val Asn
 50 55 60

Glu Leu Gly Arg Pro Ala Arg Asp Glu Gly Gly Ser Gly Arg Asp
65 70 75

Trp Lys Ser Lys Ser Gly Arg Gly Leu Ala Gly Arg Glu Pro Trp
80 85 90

Ser Lys Leu Lys Gln Ala Trp Val Ser Gln Gly Gly Gly Ala Lys
95 100 105

Ala Gly Asp Leu Gln Val Arg Pro Arg Gly Asp Thr Pro Gln Ala
110 115 120

Glu Ala Leu Ala Ala Ala Ala Gln Asp Ala Ile Gly Pro Glu Leu
125 130 135

Ala Pro Thr Pro Glu Pro Pro Glu Glu Tyr Val Tyr Pro Asp Tyr
140 145 150

Arg Gly Lys Gly Cys Val Asp Glu Ser Gly Phe Val Tyr Ala Ile
155 160 165

Gly Glu Lys Phe Ala Pro Gly Pro Ser Ala Cys Pro Cys Leu Cys
170 175 180

Thr Glu Glu Gly Pro Leu Cys Ala Gln Pro Glu Cys Pro Arg Leu
185 190 195

His Pro Arg Cys Ile His Val Asp Thr Ser Gln Cys Cys Pro Gln
200 205 210

Cys Lys Glu Arg Lys Asn Tyr Cys Glu Phe Arg Gly Lys Thr Tyr
215 220 225

Gln Thr Leu Glu Glu Phe Val Val Ser Pro Cys Glu Arg Cys Arg
230 235 240

Cys Glu Ala Asn Gly Glu Val Leu Cys Thr Val Ser Ala Cys Pro
245 250 255

Gln Thr Glu Cys Val Asp Pro Val Tyr Glu Pro Asp Gln Cys Cys
260 265 270

Pro Ile Cys Lys Asn Gly Pro Asn Cys Phe Ala Glu Thr Ala Val
275 280 285

Ile Pro Ala Gly Arg Glu Val Lys Thr Asp Glu Cys Thr Ile Cys
290 295 300

His Cys Thr Tyr Glu Glu Gly Thr Trp Arg Ile Glu Arg Gln Ala
305 310 315

Met Cys Thr Arg His Glu Cys Arg Gln Met
320 325

<210> 12

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic Oligonucleotide Probe

<400> 12

gaggtgtcgc tgtgaagcca acgg 24

<210> 13

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic Oligonucleotide Probe

<400> 13

cgctcgattc tccatgtgcc ttcc 24

<210> 14

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic Oligonucleotide Probe

SECRET

gacggagtgt gtggacctg tgtacgagcc tgatcagtgc tgtcc 45

<210> 15

<211> 1587

<212> DNA

<213> Homo sapiens

<400> 15

cagccacaga cgggtcatga gcgcggtatt actgctggcc ctctgggggt 50

tcatectccc actgccagga gtgcaggcgc tgctctgcc a gtttgggaca 100

gttcagcatg tgtggaaggt gtccgaccta ccccggcaat ggaccacctaa 150

gaacaccagc tgcgacagcg gcttgggggtg ccaggacacg ttgatgctca 200

ttgagagcgg accccaagtg agcctggtgc tctccaaggg ctgcacggag 250

gccaaaggacc aggagccccg cgtcactgag caccggatgg gccccggcct 300

ctccctgac tctacacct tctgtgccg ccaggaggac ttctgcaaca 350

acctcgtaa ctccctcccg ctttgggccc cacagccccc agcagaccca 400

ggatccttga ggtgccagc ctgctgtct atggaaggc gtctggagg 450

gacaacagaa gagatctgcc ccaaggggac cacacactgt tatgatggcc 500

tcttcaggct caggggagga ggcattctt ccaatctgag agtccaggga 550

tgcatgcccc agccaggttg caacctgctc aatgggacac aggaaattgg 600

gcccgtgggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650

atcggggggac caccattatg acacacggaa acttggctca agaaccact 700

gattggacca catcgaatac cgagatgtgc gaggtggggc aggtgtgtca 750

ggagacgctg ctgctcatag atgtaggact cacatcaacc ctggtgggga 800

caaaaggctg cagcactgtt ggggctcaaa attcccagaa gaccaccatc 850

cactcagccc ctctgggggt gcttgtggcc tcctataccc acttctgctc 900

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

<211> 437

<213> Hom

Met Ser Al

1

Asn Thr Ser

Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly
65 70 75

Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
80 85 90

Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
95 100 105

Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
110 115 120

Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
125 130 135

Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
140 145 150

Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu
155 160 165

Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met
170 175 180

Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly
185 190 195

Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr
200 205 210

Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln
215 220 225

Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val
230 235 240

Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu
245 250 255

Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala
260 265 270

Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val
275 280 285

Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn
 290 295 300

Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln
 305 310 315

Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln
 320 325 330

Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro
 335 340 345

Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly
 350 355 360

Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln
 365 370 375

Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe
 380 385 390

Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His
 395 400 405

Glu Gly Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val
 410 415 420

Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro
 425 430 435

Ser Cys

<210> 17

<211> 2387

<212> DNA

<213> Homo sapiens

<400> 17

cgacgatgct acgcgcgccc ggctgcctcc tccggacctc cgtagcgcct 50

gccgcggccc tggctgcggc gctgctctcg tcgcttgcgc gctgctctct 100

tctagagccg agggacccgg tggcctcgtc gctcagcccc tatttcggca 150

ccgagtgcag atgttattaa atgaaaaggt gttaccttg gcttactcac 1350
aagaaactgt ttcatfittat gaagatctga agaaccacta caaggacatc 1400
cttcagagtt gtcaaaccag tgaagaatgt gaattagcaa gggctaacag 1450
tacatctgat gaactatgag taactgaaga acatttttaa ttcttttagga 1500
atctgcaatg agtgattaca tgcttgtaat aggtaggcaa ttccttgatt 1550
acaggaagct ttatattac ttgagtattt ctgtcttttc acagaaaaac 1600
attgggttct tctctgggtt tggacatgaa atgaagaaa agatttttca 1650
ctggagcagc tctcttaagg agaaacaaat ctatttagag aaacagctgg 1700
ccctgcaaat gtttacagaa atgaaattct tctactttat ataagaaatc 1750
tcacactgag atagaattgt gatttcataa taacacttga aaagtctgg 1800
agtaacaaaa tatctcagtt ggaccatcct taacttgatt gaactgtcta 1850
ggaactttac agattgttct gcagttctct ctctttttcc tcaggttagga 1900
cagctctagc attttcttaa tcaggaatat tgtggttaagc tgggagtatc 1950
actctggaag aaagtaacat ctccagatga gaatttgaaa caagaaacag 2000
agtgttgtaa aaggacacct tcaactgaagc aagtcggaaa gtacaatgaa 2050
aataaatatt ttgggtattt atttatgaaa tatttgaaca tttttcaat 2100
aattcctttt tacttctagg aagtcctaaa agaccatctt aaattattat 2150
atgtttggac aattagcaac aagtcagata gtagaatcg aagtttttca 2200
aatccattgc ttagctaact tttaattct gtcacttggc ttcgattttt 2250
atattttcct attatatgaa atgtatcttt tggttgtttg attttcttt 2300
ctttctttgt aaatagttct gagttctgtc aaatgccgtg aaagtatttg 2350
ctataataaa gaaaattctt gtgactttaa aaaaaaa 2387

<211> 487

<212> PRT

<213> Homo sapiens

<400> 18

Met Leu Arg Ala Pro Gly Cys Leu Leu Arg Thr Ser Val Ala Pro
1 5 10 15

Ala Ala Ala Leu Ala Ala Ala Leu Leu Ser Ser Leu Ala Arg Cys
20 25 30

Ser Leu Leu Glu Pro Arg Asp Pro Val Ala Ser Ser Leu Ser Pro
35 40 45

Tyr Phe Gly Thr Lys Thr Arg Tyr Glu Asp Val Asn Pro Val Leu
50 55 60

Leu Ser Gly Pro Glu Ala Pro Trp Arg Asp Pro Glu Leu Leu Glu
65 70 75

Gly Thr Cys Thr Pro Val Gln Leu Val Ala Leu Ile Arg His Gly
80 85 90

Thr Arg Tyr Pro Thr Val Lys Gln Ile Arg Lys Leu Arg Gln Leu
95 100 105

His Gly Leu Leu Gln Ala Arg Gly Ser Arg Asp Gly Gly Ala Ser
110 115 120

Ser Thr Gly Ser Arg Asp Leu Gly Ala Ala Leu Ala Asp Trp Pro
125 130 135

Leu Trp Tyr Ala Asp Trp Met Asp Gly Gln Leu Val Glu Lys Gly
140 145 150

Arg Gln Asp Met Arg Gln Leu Ala Leu Arg Leu Ala Ser Leu Phe
155 160 165

Pro Ala Leu Phe Ser Arg Glu Asn Tyr Gly Arg Leu Arg Leu Ile
170 175 180

Thr Ser Ser Lys His Arg Cys Met Asp Ser Ser Ala Ala Phe Leu
185 190 195

Gln Gly Leu Trp Gln His Tyr His Pro Gly Leu Pro Pro Pro Asp

09660405601

200 205 210

Val Ala Asp Met Glu Phe Gly Pro Pro Thr Val Asn Asp Lys Leu
215 220 225

Met Arg Phe Phe Asp His Cys Glu Lys Phe Leu Thr Glu Val Glu
230 235 240

Lys Asn Ala Thr Ala Leu Tyr His Val Glu Ala Phe Lys Thr Gly
245 250 255

Pro Glu Met Gln Asn Ile Leu Lys Lys Val Ala Ala Thr Leu Gln
260 265 270

Val Pro Val Asn Asp Leu Asn Ala Asp Leu Ile Gln Val Ala Phe
275 280 285

Phe Thr Cys Ser Phe Asp Leu Ala Ile Lys Gly Val Lys Ser Pro
290 295 300

Trp Cys Asp Val Phe Asp Ile Asp Asp Ala Lys Val Leu Glu Tyr
305 310 315

Leu Asn Asp Leu Lys Gln Tyr Trp Lys Arg Gly Tyr Gly Tyr Thr
320 325 330

Ile Asn Ser Arg Ser Ser Cys Thr Leu Phe Gln Asp Ile Phe Gln
335 340 345

His Leu Asp Lys Ala Val Glu Gln Lys Gln Arg Ser Gln Pro Ile
350 355 360

Ser Ser Pro Val Ile Leu Gln Phe Gly His Ala Glu Thr Leu Leu
365 370 375

Pro Leu Leu Ser Leu Met Gly Tyr Phe Lys Asp Lys Glu Pro Leu
380 385 390

Thr Ala Tyr Asn Tyr Lys Lys Gln Met His Arg Lys Phe Arg Ser
395 400 405

Gly Leu Ile Val Pro Tyr Ala Ser Asn Leu Ile Phe Val Leu Tyr
410 415 420

His Cys Glu Asn Ala Lys Thr Pro Lys Glu Gln Phe Arg Val Gln

425 430 435

Met Leu Leu Asn Glu Lys Val Leu Pro Leu Ala Tyr Ser Gln Glu
440 445 450

Thr Val Ser Phe Tyr Glu Asp Leu Lys Asn His Tyr Lys Asp Ile
455 460 465

Leu Gln Ser Cys Gln Thr Ser Glu Glu Cys Glu Leu Ala Arg Ala
470 475 480

Asn Ser Thr Ser Asp Glu Leu
485

<210> 19

<211> 3554

<212> DNA

<213> Homo sapiens

<400> 19

gggactacaa gccgcgccgc gctgccgctg gccctcagc aaccctcgac 50

atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100

cttcttctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150

tcaaatccag caatcgaacc ccagtggtag aggaattga aagtgtggaa 200

ctgtcttga tcattacgga ttcgcagaca agtgaccca ggatcgagt 250

gaagaaaatt caagatgaac aaaccacata tgtgttttt gacaacaaaa 300

ttcagggaga ctggcgggt cgtgcagaaa tactggggaa gacatccctg 350

aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400

cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450

ctgtgcaagt gaagccagt acccctgtct gtagagtgcc gaaggctgta 500

ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550

ccggcctcac tacagctggt atcgcaatga tgtaccactg cccacggatt 600

ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650

acaggcactt tggtgttcac tgctgttcac aaggacgact ctgggcagta 700
ctactgcatt gcttccaatg acgcaggctc agccagggtg gaggagcagg 750
agatggaagt ctatgacctg aacattggcg gaattattgg ggggggttctg 800
gttgctcttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850
cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900
accaggga accagatgga gtaactaca tccgactga cgaggagggc 950
gacttcagac acaagtcac gtttgtgac tgagaccgc ggtgtggctg 1000
agagcgcaca gagcgcacgt gcacatacct ctgctagaaa ctctgtcaa 1050
ggcagcgaga gctgatgcac tcggacagag ctagacactc attcagaagc 1100
tttctgttt ggccaaagt gaccactact cttcttactc taacaagcca 1150
catgaataga agaattttcc tcaagatgga cccggtaaataa accacaca 1200
ggaagcgaaa ctgggtgcgt tctactgagtt gggttcctaa tctgtttctg 1250
gcctgattcc cgcatgagta ttagggtgat cttaaagagt ttgctcacgt 1300
aaacgcccgt gctgggccct gtgaagccag catgttcacc actggtcgtt 1350
cagcagccac gacagcacca tgtgagatgg cgagggtggc ggacagcacc 1400
agcagcgcat cccggcgga accagaaaa ggcttcttac acagcagcct 1450
tacttcacg gccacagac accaccgag tttctctta aaggctctgc 1500
tgatcgggtg tgcagtgtcc attgtggaga agctttttgg atcagcattt 1550
tgtaaaaaca accaaaatca ggaaggtaaa ttggttgctg gaagagggat 1600
cttgctgag gaacctgct tgcacaacag ggtgtcagga ttaagga 1650
accttcgtct taggctaagt ctgaaatggt actgaaatat gcttttctat 1700
gggtcttgtt tattttataa aattttacat cttaaatttt gctaaggatg 1750
tattttgatt attgaaaaga aaatttctat ttaaactgta aatatattgt 1800

catacaatgt taaataacct attttttaa aaaagttcaa cttaggtag 1850
aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900
ttttacccaa ggaatcctct catggaagtt tactgtgatg ttcttttct 1950
cacacaagtt ttagcctttt tcacaaggga actcactg tctacacatc 2000
agaccatagt tgcttaggaa accttataaa attccagta agcaatgtg 2050
aaatcagttt gcactcttc aaaagaaacc tctcaggta gctttgaact 2100
gcctcttct gagatgacta ggacagtctg taccagagg ccaccagaa 2150
gccctcagat gtacatacac agatgccagt cagctcctgg ggtgcgcca 2200
ggcgccccg ctctagctca ctgtgcctc gctgtctgcc aggaggcct 2250
gccatccttg ggcctggca gtggctgtgt ccagtgagc ttactcacg 2300
tgcccttgc tcatccagc acagctctca ggtgggact gcaggacac 2350
tggtgtctc catgtagcgt ccagctttg ggctctgta acagacctt 2400
tttgggtat ggatggctca caaataggg ccccaatgc tttttttt 2450
tttaagttt gttaattat ttgtaagat tgtctaaggc caaaggcaat 2500
tgcgaaatca agtctgtcaa gtacaataac attttaaaa gaaaatgat 2550
ccactgttc ctcttgcca cagagaaagc accagacgc cacaggctt 2600
gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagccttt 2650
aaagaacgtc aggtggagca gccaggtgaa aggctggcg gggaggaaag 2700
tgaaacgcct gaatcaaaag cagtttcta atttgactt taaattttc 2750
atccgccgga gacactgctc ccattgtgg ggggacatta gcaacatcac 2800
tcagaagcct gtgtctca agagcagtg ttctcagcct cacatgcct 2850
gccgtgctgg actcaggact gaagtgtgt aaagcaagga gctgctgaga 2900
aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcacctgt 2950

cttcagctt ccagtgtctt gggttttta tactttgaca gcttttttt 3000

aattgcatac atgagactgt gttgactttt ttagttatg tgaacactt 3050

tgccgcaggc cgcctggcag aggccaggaaa tgctccagca gtggtcagt 3100

gctccctggg gtctgtgca tggcatcctg gatgcttagc atgcaagttc 3150

cctccatcat tgccacctg gtagagaggg atggctcccc accctcagcg 3200

ttggggattc acgtccagc ctcttcttg gttgtcatag tgatagggta 3250

gccttattgc cccctcttet tataccctaa aaccttctac actagtcca 3300

tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350

gtagctgcct ataactgaga ctgacggaa aaggaatact cgtgtattt 3400

aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450

gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500

caccgtaatt tggcatttgt ttaacctcat ttataaaagc ttcaaaaaa 3550

ccca 3554

<210> 20

<211> 310

<212> PRT

<213> Homo sapiens

<400> 20

Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu

1 5 10 15

Pro Asp Phe Phe Leu Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly

20 25 30

Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu

35 40 45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr

50 55 60

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr

65	70	75
Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly		
80	85	90
Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val		
95	100	105
Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg		
110	115	120
Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val		
125	130	135
Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val		
140	145	150
Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly		
155	160	165
His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu		
170	175	180
Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe		
185	190	195
His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His		
200	205	210
Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala		
215	220	225
Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu		
230	235	240
Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val		
245	250	255
Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly		
260	265	270
Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro		
275	280	285
Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly		

290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310

<210> 21

<211> 3437

<212> DNA

<213> Homo sapiens

<400> 21

caggaccagg tcttctacg ctggagcagc ggggagacag ccacatgca 50

catcctcgtg gtccatgcca tggatgcct gctgacgctg ggcccgcctc 100

gagccgacga cagcgagttc caggcgctgc tggacatctg gtttccggag 150

gagaagccac tgcccaccgc ctctctggtg gacacatcgg aggaggcgct 200

gctgcttct gactggctga agctgcgcat gatccgttct gagtgctcc 250

gcctggtgga cgccgccctg caggacctgg agccgcagca gctgctgctg 300

ttcgtgcagt cgtttggcat cccctgttcc agcatgagca aactctcca 350

gttctggac caggcagtgg cccacgacc ccagactctg gagcagaaca 400

tcatggacaa gaattacatg gcccacctgg tggaggcca gcatgagcgc 450

ggcgctccg gaggccagac ttccactcc ttgtcacag cctccctgcc 500

gccccgccga gacagcacag aggcacccaa accaaagagc agcccagagc 550

agcccatagg ccagggccgg attcgggtgg ggaccagct ccgggtgctg 600

ggcctgagg acgacctggc tggcatgttc ctccagattt tcccgtcag 650

cccggaccct cgttggcaga gctccagtc ccgccccgtg gccctcgccc 700

tgcagcaggc cctgggccag gagctggccc gcgtcgtcca gggcagcccc 750

gagtgccgg gcatcacggt gcgtgtcctg caggccctcg ccacctgct 800

cagtcacca cacggcgtg cctggtgat gtccatgcac cgtagccact 850

056603405604

tcctggcctg cccgctgctg cgccagctct gccagtacca gcgctgtgtg 900
 ccacaggaca ccggtcttc ctcgctcttc ctgaaggtgc tcctgcagat 950
 gctgcagtgg ctggacagcc ctggcgtgga gggcgggccc ctgcgggcac 1000
 agctcaggat gcttgccagc caggcctcag ccgggcgcag gctcagtgat 1050
 gtgcgagggg ggctcctgcg cctggccgag gccctggcct tccgtcagga 1100
 cctggaggtg gtcagctcca ccgtccgtgc cgtcatgcc accctgaggt 1150
 ctggggagca gtgcagcgtg gagccggacc tgatcagcaa agtcctccag 1200
 gggctgatcg aggtgaggtc cccccacctg gaggagctgc tgactgcatt 1250
 cttctctgcc actgcggatg ctgcctcccc gtttcagcc tgtaagcccg 1300
 ttgtggtggt gagctccctg ctgctgcagg aggaggagcc cctggctggg 1350
 gggaagccgg gtgcggacgg tggcagcctg gaggccgtgc ggctggggcc 1400
 ctctcagggc ctctagtgg actggctgga aatgctggac cccgaggtgg 1450
 tcagcagctg ccccgacctg cagctcaggc tgctcttctc ccggaggaag 1500
 ggcaaaggtc aggcccaggt gccctcgttc cgtccctacc tctgacct 1550
 cttcacgcat cagtcagct ggcccacact gcaccagtgc atccgagtcc 1600
 tgctgggcaa gagccgggaa cagaggttcg acccctctgc ctctctggac 1650
 ttctctggg cctgcateca tgttctcgc atctggcagg ggcgggacca 1700
 gcgcaccccg cagaagcggc gggaggagct ggtgctgcgg gtccagggcc 1750
 cggagctcat cagcctggtg gagctgatcc tggccgaggc ggagacgcgg 1800
 agccaggacg gggacacage cgctgcage ctcatccagg cccggctgcc 1850
 cctgctgctc agctgctgct gtggggacga tgagagtgc aggaaggtga 1900
 cggagcacct gtcaggctgc atccagcagt ggggagacag cgtgctggga 1950
 aggcgctgcc gagacctct cctgcagtc tacctacagc ggccggagct 2000

gcgggtgccc gtgcctgagg tctactgca cagegaaggg gctgccagca 2050

gcagcgtctg caagctggac ggactcatcc accgcttcat cacgtcctt 2100

gcggacacca gcgactcccg ggcgttggag aaccgagggg cggatgccag 2150

catggcctgc cggaagctgg cggtaggcga cccgctgctg ctgctcaggc 2200

acctgcccac gatcgcgcg ctcctgcacg gccgcacca cctcaacttc 2250

caggagtcc ggacagagaa ccacctgagc tgcctcctgc acgtgctggg 2300

cctgctggag ctgctgcagc cgcacgtgtt ccgcagcgag caccaggggg 2350

cgtgtggga ctgcctctg tcttcatcc gcctgctgct gaattacagg 2400

aagtctccc gccatctggc tgccttcac aacaagttg tgcagttcat 2450

ccataagtac attacctaca atgccccagc agccatctcc ttcctgcaga 2500

agcacgccga cccgctccac gacctgtcct tcgacaacag tgacctggtg 2550

atgctgaaat cctccttgc agggctcagc ctgccagca gggacgacag 2600

gaccgaccga ggcctggacg aagagggcga ggaggagagc tcagccggct 2650

ccttgccct ggtcagcgtc tcctgttca cccctctgac cgcggccgag 2700

atggccctt acatgaaacg gcttcccgg ggccaaacgg tggaggatct 2750

gctggagggt ctgagtaca tagacgagat gtccggcgag agaccgaga 2800

tctgagctt cttctgacc aacctgcagc ggctgatgag ctggccgag 2850

gagtgttccc gcaacctgc cttcagcctg gccctgcgt ccatgcagaa 2900

cagccccagc attgcagccg ctttctgcc cacgttcatg tactgcctgg 2950

gcagccagga cttgaggtg gtgcagacgg cctccggaa cctgcctgag 3000

tacgtctcc tgtccaaga gcacgggct gtgctgctc accggcctt 3050

cctggtgggc atgtacggc agatggacc cagcgcgag atctccgagg 3100

ccctgaggat cctgcatatg gaggccgtga tgtgagcctg tggcagccga 3150

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE BIBLE

THE UNIVERSITY OF CHICAGO

THE UNIVERSITY OF CHICAGO

THE BIBLE

THE BIBLE

THE UNIVERSITY OF CHICAGO

THE UNIVERSITY OF CHICAGO

THE UNIVERSITY OF CHICAGO

THE UNIVERSITY OF CHICAGO

Gly Ala Ser Gly Gly Gln Thr Phe His Ser Leu Leu Thr Ala Ser
140 145 150

Leu Pro Pro Arg Arg Asp Ser Thr Glu Ala Pro Lys Pro Lys Ser
155 160 165

Ser Pro Glu Gln Pro Ile Gly Gln Gly Arg Ile Arg Val Gly Thr
170 175 180

Gln Leu Arg Val Leu Gly Pro Glu Asp Asp Leu Ala Gly Met Phe
185 190 195

Leu Gln Ile Phe Pro Leu Ser Pro Asp Pro Arg Trp Gln Ser Ser
200 205 210

Ser Pro Arg Pro Val Ala Leu Ala Leu Gln Gln Ala Leu Gly Gln
215 220 225

Glu Leu Ala Arg Val Val Gln Gly Ser Pro Glu Val Pro Gly Ile
230 235 240

Thr Val Arg Val Leu Gln Ala Leu Ala Thr Leu Leu Ser Ser Pro
245 250 255

His Gly Gly Ala Leu Val Met Ser Met His Arg Ser His Phe Leu
260 265 270

Ala Cys Pro Leu Leu Arg Gln Leu Cys Gln Tyr Gln Arg Cys Val
275 280 285

Pro Gln Asp Thr Gly Phe Ser Ser Leu Phe Leu Lys Val Leu Leu
290 295 300

Gln Met Leu Gln Trp Leu Asp Ser Pro Gly Val Glu Gly Gly Pro
305 310 315

Leu Arg Ala Gln Leu Arg Met Leu Ala Ser Gln Ala Ser Ala Gly
320 325 330

Arg Arg Leu Ser Asp Val Arg Gly Gly Leu Leu Arg Leu Ala Glu
335 340 345

Ala Leu Ala Phe Arg Gln Asp Leu Glu Val Val Ser Ser Thr Val
350 355 360

Arg Ala Val Ile Ala Thr Leu Arg Ser Gly Glu Gln Cys Ser Val
365 370 375

Glu Pro Asp Leu Ile Ser Lys Val Leu Gln Gly Leu Ile Glu Val
380 385 390

Arg Ser Pro His Leu Glu Glu Leu Leu Thr Ala Phe Phe Ser Ala
395 400 405

Thr Ala Asp Ala Ala Ser Pro Phe Pro Ala Cys Lys Pro Val Val
410 415 420

Val Val Ser Ser Leu Leu Leu Gln Glu Glu Glu Pro Leu Ala Gly
425 430 435

Gly Lys Pro Gly Ala Asp Gly Gly Ser Leu Glu Ala Val Arg Leu
440 445 450

Gly Pro Ser Ser Gly Leu Leu Val Asp Trp Leu Glu Met Leu Asp
455 460 465

Pro Glu Val Val Ser Ser Cys Pro Asp Leu Gln Leu Arg Leu Leu
470 475 480

Phe Ser Arg Arg Lys Gly Lys Gly Gln Ala Gln Val Pro Ser Phe
485 490 495

Arg Pro Tyr Leu Leu Thr Leu Phe Thr His Gln Ser Ser Trp Pro
500 505 510

Thr Leu His Gln Cys Ile Arg Val Leu Leu Gly Lys Ser Arg Glu
515 520 525

Gln Arg Phe Asp Pro Ser Ala Ser Leu Asp Phe Leu Trp Ala Cys
530 535 540

Ile His Val Pro Arg Ile Trp Gln Gly Arg Asp Gln Arg Thr Pro
545 550 555

Gln Lys Arg Arg Glu Glu Leu Val Leu Arg Val Gln Gly Pro Glu
560 565 570

Leu Ile Ser Leu Val Glu Leu Ile Leu Ala Glu Ala Glu Thr Arg
575 580 585

Ser Gln Asp Gly Asp Thr Ala Ala Cys Ser Leu Ile Gln Ala Arg
590 595 600

Leu Pro Leu Leu Leu Ser Cys Cys Cys Gly Asp Asp Glu Ser Val
605 610 615

Arg Lys Val Thr Glu His Leu Ser Gly Cys Ile Gln Gln Trp Gly
620 625 630

Asp Ser Val Leu Gly Arg Arg Cys Arg Asp Leu Leu Leu Gln Leu
635 640 645

Tyr Leu Gln Arg Pro Glu Leu Arg Val Pro Val Pro Glu Val Leu
650 655 660

Leu His Ser Glu Gly Ala Ala Ser Ser Ser Val Cys Lys Leu Asp
665 670 675

Gly Leu Ile His Arg Phe Ile Thr Leu Leu Ala Asp Thr Ser Asp
680 685 690

Ser Arg Ala Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys
695 700 705

Arg Lys Leu Ala Val Ala His Pro Leu Leu Leu Leu Arg His Leu
710 715 720

Pro Met Ile Ala Ala Leu Leu His Gly Arg Thr His Leu Asn Phe
725 730 735

Gln Glu Phe Arg Gln Gln Asn His Leu Ser Cys Phe Leu His Val
740 745 750

Leu Gly Leu Leu Glu Leu Leu Gln Pro His Val Phe Arg Ser Glu
755 760 765

His Gln Gly Ala Leu Trp Asp Cys Leu Leu Ser Phe Ile Arg Leu
770 775 780

Leu Leu Asn Tyr Arg Lys Ser Ser Arg His Leu Ala Ala Phe Ile
785 790 795

Asn Lys Phe Val Gln Phe Ile His Lys Tyr Ile Thr Tyr Asn Ala
800 805 810

Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala Asp Pro Leu His
815 820 825

Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu Lys Ser Leu
830 835 840

Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr Asp Arg
845 850 855

Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser Leu
860 865 870

Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu
875 880 885

Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu
890 895 900

Asp Leu Leu Glu Val Leu Ser Asp Ile Asp Glu Met Ser Arg Arg
905 910 915

Arg Pro Glu Ile Leu Ser Phe Phe Ser Thr Asn Leu Gln Arg Leu
920 925 930

Met Ser Ser Ala Glu Glu Cys Cys Arg Asn Leu Ala Phe Ser Leu
935 940 945

Ala Leu Arg Ser Met Gln Asn Ser Pro Ser Ile Ala Ala Ala Phe
950 955 960

Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln Asp Phe Glu Val
965 970 975

Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala Leu Leu Cys
980 985 990

Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly
995 1000 1005

Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu
1010 1015 1020

Arg Ile Leu His Met Glu Ala Val Met
1025

<210> 23
<211> 2186
<212> DNA
<213> Homo sapiens

<400> 23
ccgggcatg cagcctcggc cccgcgggcg cccgccgcgc acccgaggag 50
atgaggetcc gcaatggcac ctctctgacg ctgctgctct tctgcctgtg 100
cgccctctc tcgctgtcct ggtacgcggc actcagcggc cagaaaggcg 150
acgttgtgga cgttaccag cgggagttcc tggcgtgctg cgatcggttg 200
cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggt 250
gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgcgagacg 300
gagacggcaa tcgcacctgg ggccgcctaa cagaggaccc ccgattgaag 350
ccgtggaacg gctcacaccg gcacgtgctg cacctgccca ccgtcttcca 400
tcacctgcca cacctgctgg ccaaggagag cagtctgcag cccgcgggtg 450
gcgtgggcca gggccgcacc ggagtgtcgg tggatgagg catcccgagc 500
gtgcggcgcg aggtgcactc gtacctgact gacactctgc actcgctcat 550
ctccgagctg agcccgagg agaaggagga ctcggtcagc gtggtgctga 600
tcgccgagac tgactcacag tacacttcgg cagtgcaga gaacatcaag 650
gccttgttcc ccacggagat ccattctggg ctctggagg tcatttcacc 700
ctccccccac ttctacctg acttctcccg cctccgagag tccttgggg 750
acccaagga gagagtcagg tggaggacca aacagaacct cgattactgc 800
ttctcatga tgtacgcga gtccaaaggc atctactacg tgcagctgga 850
ggatgacatc gtggccaagc ccaactacct gagcaccatg aagaacttg 900
cactgcagca gccttcagag gactggatga tcctggagt ctcccagctg 950
ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 1000

gttcattctc atgttctacc gggacaagcc catcgactgg ctcttgacc 1050
atattctgtg ggtgaaagtc tgcaaccccg agaaggatgc gaagcactgt 1100
gaccggcaga aagccaacct gcggatccgc ttcaaaccgt ccctcttcca 1150
gcacgtgggc actcactcct cgctggctgg caagatccag aaactgaagg 1200
acaaagactt tggaaagcag gcgctgcgga aggagcatgt gaaccgcca 1250
gcagaggtga gcacgagcct gaagacatac cagcacttca ccctggagaa 1300
agcctacctg cgcgaggact tcttctgggc cttcaccct gccgcggggg 1350
acttcacccg cttccgttc ttcaacctc taagactgga gcggttctc 1400
ttccgcagtg ggaacatcga gcacccggag gacaagctct tcaacacgtc 1450
tgtggaggtg ctgcccttcg acaaccctca gtcagacaag gaggcctgc 1500
aggagggccg caccgccacc ctccgtacc ctccgagccc cgacggctac 1550
ctccagatcg gctccttcta caaggagtg gcagaggag aggtggacce 1600
agccttcggc cctctggaag cactgcgcct ctgatccag acggactccc 1650
ctgtgtgggt gattctgagc gagatcttc tgaaaaaggc cgactaagct 1700
gcgggcttct gagggtacce tgtggccagc cctgaagccc acatttctgg 1750
gggtgtcgtc actgccgtcc ccggagggcc agatacggcc ccgccc aaag 1800
ggttctgcct ggcgtcgggc ttgggccggc ctgggggtccg ccgctggccc 1850
ggaggcccta ggagctgggt ctgccccgc ccgccgggcc gcggaggagg 1900
caggcgcccc ccacactgt cctgaggccc ggaaccgttc gcacccggcc 1950
tgccccagtc aggccgtttt agaagagctt ttacttgggc gcccgccgtc 2000
tctggcgcca acactggaat gcatatacta ctttatgtgc tgtgttttt 2050
attcttgat acatttgatt tttcacgta agtcacata tacttctata 2100
agagcgtgac ttgtaataaa gggttaatga agaaaaaaaa aaaaaaaaaa 2150

[illegible]

<211> 548

<213> Homo sapiens

Met Arg Leu Arg Asn Gly Thr Phe Leu Thr Leu Leu Leu Phe Cys

1 5 10 15

Leu Cys Ala Phe Leu Ser Leu Ser Trp Tyr Ala Ala Leu Ser Gly

20 25 30

Gln Lys Gly Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala

35 40 45

Leu Arg Asp Arg Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg

50 55 60

Ser Lys Glu Leu Asn Leu Val Leu Asp Glu Ile Lys Arg Ala Val

65 70 75

Ser Glu Arg Gln Ala Leu Arg Asp Gly Asp Gly Asn Arg Thr Trp

80 85 90

Gly Arg Leu Thr Glu Asp Pro Arg Leu Lys Pro Trp Asn Gly Ser

95 100 105

His Arg His Val Leu His Leu Pro Thr Val Phe His His Leu Pro

110 115 120

His Leu Leu Ala Lys Glu Ser Ser Leu Gln Pro Ala Val Arg Val

125 130 135

Gly Gln Gly Arg Thr Gly Val Ser Val Val Met Gly Ile Pro Ser

140 145 150

Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp Thr Leu His Ser

155 160 165

Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp Ser Val Ile

170 175 180

Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser Ala Val

185 190 195

Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser Gly
200 205 210

Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe
215 220 225

Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg
230 235 240

Trp Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr
245 250 255

Ala Gln Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile
260 265 270

Val Ala Lys Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu
275 280 285

Gln Gln Pro Ser Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu
290 295 300

Gly Phe Ile Gly Lys Met Phe Lys Ser Leu Asp Leu Ser Leu Ile
305 310 315

Val Glu Phe Ile Leu Met Phe Tyr Arg Asp Lys Pro Ile Asp Trp
320 325 330

Leu Leu Asp His Ile Leu Trp Val Lys Val Cys Asn Pro Glu Lys
335 340 345

Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn Leu Arg Ile Arg
350 355 360

Phe Lys Pro Ser Leu Phe Gln His Val Gly Thr His Ser Ser Leu
365 370 375

Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys Asp Phe Gly Lys Gln
380 385 390

Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala Glu Val Ser Thr
395 400 405

Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr Leu

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-41

<223> Synthetic Oligonucleotide Probe

<400> 26

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 27

<211> 19

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-19

<223> Synthetic Oligonucleotide Probe

<400> 27

actcgggatt cctgctgtt 19

<210> 28

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic Oligonucleotide Probe

<400> 28

aggcctttac ccaaggccac aac 23

<210> 29

<211> 19

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-19

<223> Synthetic Oligonucleotide Probe

<400> 29

ggcctgtcct gtgttctca 19

<210> 30

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic Oligonucleotide Probe

<400> 30

tcccaccact tacttccatg aa 22

<210> 31

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic Oligonucleotide Probe

<400> 31

ctgtggtacc caattgccgc ctgtg 25

<210> 32

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic Oligonucleotide Probe

<400> 32

attgtcctga gattcgagca aga 23

<210> 33

<211> 18

<212> DNA

TC9250-409860

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic Oligonucleotide Probe

<400> 33

gtccagcaag ccctcatt 18

<210> 34

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic Oligonucleotide Probe

<400> 34

cttctgggcc acagccctgc 20

<210> 35

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic Oligonucleotide Probe

<400> 35

cagttcaggt cgtttcatc a 21

<210> 36

<211> 19

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-19

<223> Synthetic Oligonucleotide Probe

<400> 36
ccagtcaggc cgttttaga 19

<210> 37
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic Oligonucleotide Probe

<400> 37
cgggcgcca agtaaaagct c 21

<210> 38
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic Oligonucleotide Probe

<400> 38
cataaagtag tatatgcatt ccagtgtt 28

TE099950-4E099950